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(a) preparing a test nucleic acid corresponding to the region;

10 complementary to the normal sequence;

(d) reacting the test nucleic acid with the probes
15 on the DNA array substrate;

20 (f) determining the presence or absence of
mutation in the test nucleic acid comparing with a
histogram pattern of signals of all regions obtained
using a normal sample without variation.

2. The method according to claim 1, wherein the signal is a light emitted from each hybrid and the total signal is measured as a total light quantity

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~~emitted from each region.~~

3. The method according to claim 2, wherein the light is fluorescence.

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4. The method according to claim 2, wherein the light is a chemical luminescence.

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~~5. The method according to claim 1, wherein the steps (c) to (e) are:~~

(c) preparing separated regions on a substrate by fixing probes on a surface of the substrate, wherein the separate regions comprises:

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a first region containing probes which provide a signal of a certain intensity on reaction with a nucleic acid having normal sequence,

a second region containing probes which provide weaker signals on reaction with a nucleic acid having normal sequence, and

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the third region containing probes which do not form hybrids on reaction with a nucleic acid having normal sequence;

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(d) reacting the DNA array of step (c) with a nucleic acid having normal sequence and measuring a signal of at least one region selected from the three regions to obtain a first pattern; and

reacting the DNA array of step (c) with the test

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~~nucleic acid, and measuring a signals of at least one~~
region corresponding to the selected region of the step
(d) to obtain a second pattern; and

(e) determining the presence or absence of
5 variation in the test nucleic acid by comparing the
first and second patterns.

6. The method according to claim 5, wherein the
selected region is the first region giving a strongest
10 total signal and/or the third region giving no or a
weakest signal on reaction with a nucleic acid having
normal sequence.

7. The method according to claim 5, wherein the
15 separate regions are arranged on the substrate in order
of signal intensity obtainable by reacting with a
nucleic acid having normal sequence, from the highest
intensity to the lowest intensity along a direction of
a detection.

20 8. The method according to claim 5, wherein the
selected region is the third region, and when a total
signal is detected with the test nucleic acid in the
step (d), variation is called positive, and the test
25 nucleic acid is determined to have variation.

9. The method according to claim 5, wherein the

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first region contains probes consisting of a probe having a fully complementary sequence to the normal sequence and probes having one-base mismatch to the normal sequence. When reacting with a normal base sequence of a nucleic acid.

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10. The method according to claim 5, wherein the selected regions are both of the first and the third region and determining the presence or absence of variation comparing the ratio of the intensity of the third region to that of the first region.

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11. The method according to claim 5, wherein the selected regions are all of the region, and determined the presence or absence of variation comparing the histogram pattern of signal intensity.

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12. The method according to claim 5, wherein detection of the total signal is performed by an area sensor.

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13. The method according to claim 7, wherein detection of the total signal is performed by a line sensor.

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14. The method according to claim 1, wherein a base length of the probes is 8 mer to 30 mer.

15. The method according to claim 14, wherein the base length of the probes is 12 mer to 25 mer.

16. A DNA array substrate for screening a variation in a region of a nucleic acid, wherein a full match probe fully complementary to a normal sequence of the region, and a plurality of mismatch probes having at least one base mismatch to the sequence are arranged on the substrate; and

the probes are arranged to form at least two separate regions selected from:

a first region containing at least one probe which provides a signal of a certain intensity on reaction with a nucleic acid having the normal sequence,

a second region containing at least one probe which provides a weaker signal than the probe of the first region on reaction with a nucleic acid having normal sequence, and

the third region containing at least one probe which provides no signal on reaction with a nucleic acid having normal sequence.

17. The DNA array substrate according to claim 16, wherein the signal is fluorescence.

18. The DNA array substrate according to claim 16, wherein the signal is chemical luminescence.

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19. ~~The DNA array substrate according to claim~~
16, wherein the first region contains the full match
probe and the mismatch probes having one mismatch base.
When reacting with a normal base sequence of a nucleic
5 acid.

20. The DNA array substrate according to claim
16, wherein the separate regions are arranged on the
substrate in order of total signal intensity obtainable
by reacting with a nucleic acid having normal sequence,
10 from a highest intensity to a lowest intensity along a
direction of a detection.

21. The DNA array substrate according to claim
16, wherein a length of the probes is 8 mer to 30 mer.

22. The DNA array substrate according to claim
21, wherein the length of the probes is 12 mer to 25
15 ~~mer.~~

23. A system for detecting variation comprising a
DNA array substrate according to claim 16 and a signal
measuring apparatus which measures signals from
separate regions of the DNA array substrate.

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